SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Foerderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma RIIb)

<130> 30287P_WO HC

<140> PCT/EP2004/013450
<141> 2004-11-26

<150> EP03027000.3
<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1
<211> 172
<212> PRT
<213> human

<220>
<223> Fc gamma RIIa

<400> 1

```
Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
  1               5                  10                  15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
             20                  25                  30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
         35                  40                  45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
     50                  55                  60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
 65                  70                  75                  80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
                 85                  90                  95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
            100                 105                 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
        115                 120                 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
    130                 135                 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145                 150                 155                 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
                165                 170
```

<210> 2
<211> 172
<212> PRT
<213> human

<220>
<223> Fc gamma RIIb

<400> 2

```
Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
  1               5                  10                  15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
            20                  25                  30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
        35                  40                  45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
    50                  55                  60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65                  70                  75                  80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
                85                  90                  95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
            100                 105                 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
        115                 120                 125

Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
    130                 135                 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145                 150                 155                 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
                165                 170
```

<210> 3
<211> 13
<212> PRT
<213> human

<220>
<223> glycopeptide CDE [126-137]

<400> 3

```
Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
  1               5                  10
```

<210> 4
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable light region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 4

```
aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga   48
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
  1               5                  10                  15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac   96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
             20                  25                  30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc   144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
         35                  40                  45

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc   192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
     50                  55                  60

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct   240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65                  70                  75                  80

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac   288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
                 85                  90                  95

acg ttc gga ggg ggg acc aag ctg                                  312
Thr Phe Gly Gly Gly Thr Lys Leu
            100
```

<210> 5
<211> 104
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 5

```
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
  1               5                  10                  15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
             20                  25                  30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
         35                  40                  45

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
     50                  55                  60

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65                  70                  75                  80
```

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu
100

<210> 6
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable heavy region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence comprised by an antibody

<400> 6

```
gtg cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca   48
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
  1               5                  10                  15

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat   96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
             20                  25                  30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga   144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
         35                  40                  45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag   192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
     50                  55                  60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg   240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
 65                  70                  75                  80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat   288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
                 85                  90                  95

ggt ccg ttt gct tac tgg ggc caa                                   312
Gly Pro Phe Ala Tyr Trp Gly Gln
            100
```

<210> 7
<211> 104
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: sequence comprised by an antibody

<400> 7

```
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
  1               5                  10                  15

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
            20                  25                  30

Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
        35                  40                  45

Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
    50                  55                  60

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65                  70                  75                  80

Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
                85                  90                  95

Gly Pro Phe Ala Tyr Trp Gly Gln
            100
```

<210> 8
<211> 309
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(309)
<223> variable light region of mAb CE5

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 8

```
gag ctc acc cag tct cca gcc tcc ctt tct gcg tct gtg gga gaa act   48
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
  1               5                  10                  15

gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca   96
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
            20                  25                  30

tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat   144
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
        35                  40                  45

aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga   192
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60

tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat   240
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
65                  70                  75                  80

ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cgg acg ttc   288
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
                85                  90                  95

ggt gga ggg acc aag ctc gag                                      309
```

Gly Gly Gly Thr Lys Leu Glu
100

<210> 9
<211> 103
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: sequence comprised by an antibody

<400> 9
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
20 25 30

Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
35 40 45

Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Leu Glu
100

<210> 10
<211> 339
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (3)..(338)
<223> variable heavy region of mAb CE5

<220>
<223> Description of Unknown Organism: sequence comprised by an antibody

<400> 10
tg cag gag tca gga cct ggc ctg gtg gcg ccc tca cag agc ctg tcc 47
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
1 5 10 15

atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac 95
Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
20 25 30

tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att 143
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
35 40 45

```
tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg   191
Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
          50                  55                  60

agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac   239
Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
     65                  70                  75

agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga   287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg
 80                  85                  90                  95

gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc   335
Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
                100                 105                 110

tca g                                                            339
Ser
```

<210> 11
<211> 112
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11

```
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
  1               5                  10                  15

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
             20                  25                  30

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
         35                  40                  45

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
     50                  55                  60

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
 65                  70                  75                  80

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
                 85                  90                  95

Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
            100                 105                 110
```